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#15

RAW SEQUENCE LISTING   DATE: 05/08/2002
PATENT APPLICATION: US/09/000,004A   TIME: 10:40:08

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  1 <110> APPLICANT: Tsilibary, Photini-Effie
  2       Charonis, Aristidis S.
  3       Setty, Suman
  4       Mauer, Michael
  5 <120> TITLE OF INVENTION: ANALYSIS OF ALPHA INTEGRINS FOR THE DIAGNOSIS OF DIABETIC
NEPHROPATHY
  6 <130> FILE REFERENCE: 600.314USWO
C--> 7 <140> CURRENT APPLICATION NUMBER: US/09/000,004A
  8 <141> CURRENT FILING DATE: 2001-06-19
  9 <150> PRIOR APPLICATION NUMBER: US 60/001,387
 10 <151> PRIOR FILING DATE: 1995-07-21
 11 <150> PRIOR APPLICATION NUMBER: US 60/001,861
 12 <151> PRIOR FILING DATE: 1995-08-03
 13 <150> PRIOR APPLICATION NUMBER: US 60/016,700
 14 <151> PRIOR FILING DATE: 1996-05-02
 15 <150> PRIOR APPLICATION NUMBER: PCT/US96/12067
 16 <151> PRIOR FILING DATE: 1996-07-19
 17 <160> NUMBER OF SEQ ID NOS: 16
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 21 <211> LENGTH: 3989
 22 <212> TYPE: DNA
 23 <213> ORGANISM: Rattus
 24 <220> FEATURE:
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 33       cacaggaaat cactcctcca cagctcctgg gcgcagcagc ggctggggcc actgccggac      300
 34       accctcggag accacacgag tgacccagag cgcaagtcgc cagcgtcccg gttctgcctg      360
 35       ttcctgccag ctcctgccca cgaaccggca cgtagctggt ccagcagcc gctccagca       419
 36       atg gtc ccc agg cgt cct gcc agc cta gag gtc act gta gcc tgc ata       467
 37       Met Val Pro Arg Arg Pro Ala Ser Leu Glu Val Thr Val Ala Cys Ile
 38       1               5                   10                  15
 39       tgg ctt ctc acg gtc atc cta ggc ttc tgc gtc tcc ttc aat gtt gat       515
 40       Trp Leu Leu Thr Val Ile Leu Gly Phe Cys Val Ser Phe Asn Val Asp
 41                   20                  25                  30
 42       gtg aaa aac tca atg agt ttc agt ggc cca gta gag gac atg ttt gga       563
 43       Val Lys Asn Ser Met Ser Phe Ser Gly Pro Val Glu Asp Met Phe Gly
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45   tac act gtt caa caa tat gaa aac gaa gaa ggc aaa tgg gtt ctt att      611
46   Tyr Thr Val Gln Gln Tyr Glu Asn Glu Glu Gly Lys Trp Val Leu Ile
47           50                  55                  60
48   ggt tct cct tta gtt ggc caa ccc aaa gca aga act gga gat gtc tat      659
49   Gly Ser Pro Leu Val Gly Gln Pro Lys Ala Arg Thr Gly Asp Val Tyr
50   65                  70                  75                  80
51   aag tgt ccg gtt ggg aga gag aga gca atg cct tgc gtg aag ttg gac      707
52   Lys Cys Pro Val Gly Arg Glu Arg Ala Met Pro Cys Val Lys Leu Asp
53               85                  90                  95
54   ttg cca gtt aac aca tcg atc ccc aat gtc aca gaa ata aag gaa aac      755
55   Leu Pro Val Asn Thr Ser Ile Pro Asn Val Thr Glu Ile Lys Glu Asn
56               100                 105                 110
57   atg aca ttt gga tca act tta gtc acc aac ccg aat gga gga ttt ctg      803
58   Met Thr Phe Gly Ser Thr Leu Val Thr Asn Pro Asn Gly Gly Phe Leu
59           115                 120                 125
60   gca tgt ggg ccc ttg tat gcc tat aga tgt gga cat ttg cat tat aca      851
61   Ala Cys Gly Pro Leu Tyr Ala Tyr Arg Cys Gly His Leu His Tyr Thr
62           130                 135                 140
63   act gga ata tgt tct gat gtc agt cct aca ttt caa gtt gtg aac tcc      899
64   Thr Gly Ile Cys Ser Asp Val Ser Pro Thr Phe Gln Val Val Asn Ser
65   145                 150                 155                 160
66   ttt gcc cct gta caa gaa tgc agc acc cag ctg gac ata gtc atc gtc      947
67   Phe Ala Pro Val Gln Glu Cys Ser Thr Gln Leu Asp Ile Val Ile Val
68               165                 170                 175
69   ctg gat ggc tcc aac agc atc tac ccc tgg gaa agt gtc atc gcc ttt      995
70   Leu Asp Gly Ser Asn Ser Ile Tyr Pro Trp Glu Ser Val Ile Ala Phe
71               180                 185                 190
72   tta aac gac ctt ctt aag agg atg gat att ggc cct aag cag aca cag     1043
73   Leu Asn Asp Leu Leu Lys Arg Met Asp Ile Gly Pro Lys Gln Thr Gln
74           195                 200                 205
75   gtc ggg att gta cag tat gga gag aat gta acc cat gag ttc aac ctc     1091
76   Val Gly Ile Val Gln Tyr Gly Glu Asn Val Thr His Glu Phe Asn Leu
77           210                 215                 220
78   aat aag tat tca tcc aca gaa gag gtc ctt gtc gca gca aac aaa ata     1139
79   Asn Lys Tyr Ser Ser Thr Glu Glu Val Leu Val Ala Ala Asn Lys Ile
80   225                 230                 235                 240
81   ggc cga cag gga ggc ctc caa acg atg aca gcc ctt gga ata gac aca     1187
82   Gly Arg Gln Gly Gly Leu Gln Thr Met Thr Ala Leu Gly Ile Asp Thr
83               245                 250                 255
84   gcc agg aaa gag gca ttc act gaa gct cgg ggt gcc agg agg gga gtt     1235
85   Ala Arg Lys Glu Ala Phe Thr Glu Ala Arg Gly Ala Arg Arg Gly Val
86               260                 265                 270
87   aaa aaa gtc atg gtt att gtg acc gac gga gaa tcg cat gac aac tat     1283
88   Lys Lys Val Met Val Ile Val Thr Asp Gly Glu Ser His Asp Asn Tyr
89           275                 280                 285
90   cgc ctg aaa cag gtc atc caa gac tgc gag gac gaa aac att cag cga     1331
91   Arg Leu Lys Gln Val Ile Gln Asp Cys Glu Asp Glu Asn Ile Gln Arg
92           290                 295                 300
93   ttt tcc ata gct atc ctt ggc cac tat aac agg ggg aac tta agc act     1379
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94        Phe Ser Ile Ala Ile Leu Gly His Tyr Asn Arg Gly Asn Leu Ser Thr
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96        gaa aaa ttt gtg gag gaa ata aaa tcg atc gca agc gag ccc acg gaa    1427
97        Glu Lys Phe Val Glu Glu Ile Lys Ser Ile Ala Ser Glu Pro Thr Glu
98                      ,325            330             335
99        aag cac ttc ttc aat gtc tcg gat gag ttg gcc ctg gtc act att gtt    1475
100        Lys His Phe Phe Asn Val Ser Asp Glu Leu Ala Leu Val Thr Ile Val
101                      340             345             350
102        aaa gct ctg gga gaa agg ata ttc gct ttg gaa gcg aca gct gac cag    1523
103        Lys Ala Leu Gly Glu Arg Ile Phe Ala Leu Glu Ala Thr Ala Asp Gln
104              355             360             365
105        tca gca gct tca ttt gag atg gaa atg tct cag act ggc ttc agt gct    1571
106        Ser Ala Ala Ser Phe Glu Met Glu Met Ser Gln Thr Gly Phe Ser Ala
107              370             375             380
108        cac tac tcc cag gac tgg gtc atg ctt gga gcg gtg gga gcc tat gac    1619
109        His Tyr Ser Gln Asp Trp Val Met Leu Gly Ala Val Gly Ala Tyr Asp
110        385             390             395             400
111        tgg aac gga act gtg gtc atg cag aag gct aac cag atg gtc atc cct    1667
112        Trp Asn Gly Thr Val Val Met Gln Lys Ala Asn Gln Met Val Ile Pro
113              405             410             415
114        cat aac acc acc ttt caa act gag ccc gcc aag atg aac gag cct ctg    1715
115        His Asn Thr Thr Phe Gln Thr Glu Pro Ala Lys Met Asn Glu Pro Leu
116              420             425             430
117        gct tct tat tta ggt tac aca gtg aac tcg gcc acc atc cct gga gat    1763
118        Ala Ser Tyr Leu Gly Tyr Thr Val Asn Ser Ala Thr Ile Pro Gly Asp
119              435             440             445
120        gtg ctc tac atc gct ggg cag cct cgg tac aat cat acg ggc cag gtc    1811
121        Val Leu Tyr Ile Ala Gly Gln Pro Arg Tyr Asn His Thr Gly Gln Val
122              450             455             460
123        gtc atc tac aag atg gag gat ggg aac atc aac att ctg cag aca ctc    1859
124        Val Ile Tyr Lys Met Glu Asp Gly Asn Ile Asn Ile Leu Gln Thr Leu
125        465             470             475             480
126        ggc gga gag cag att ggt tcc tac ttt ggt agt gtc tta aca aca att    1907
127        Gly Gly Glu Gln Ile Gly Ser Tyr Phe Gly Ser Val Leu Thr Thr Ile
128              485             490             495
129        gac atc gac aaa gat tct tat act gat ctg ctt ctc gtc ggg gcc ccc    1955
130        Asp Ile Asp Lys Asp Ser Tyr Thr Asp Leu Leu Leu Val Gly Ala Pro
131              500             505             510
132        atg tac atg ggg aca gag aaa gag gaa cag ggc aag gtg tac gtg tac    2003
133        Met Tyr Met Gly Thr Glu Lys Glu Glu Gln Gly Lys Val Tyr Val Tyr
134              515             520             525
135        gct gtg aat cag aca agg ttt gaa tat caa atg agc ctg gaa cca att    2051
136        Ala Val Asn Gln Thr Arg Phe Glu Tyr Gln Met Ser Leu Glu Pro Ile
137              530             535             540
138        agg cag acc tgc tgc tca tcc ctg aag gat aat tca tgc acg aaa gaa    2099
139        Arg Gln Thr Cys Cys Ser Ser Leu Lys Asp Asn Ser Cys Thr Lys Glu
140        545             550             555             560
141        aac aag aat gag ccc tgc ggg gcc cgc ttc gga aca gca att gct gct    2147
142        Asn Lys Asn Glu Pro Cys Gly Ala Arg Phe Gly Thr Ala Ile Ala Ala
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143                   565                  570                   575
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147     ccg ctg gaa gat gac cac gca gga gct gtg tac att tat cat ggc agt   2243
148     Pro Leu Glu Asp Asp His Ala Gly Ala Val Tyr Ile Tyr His Gly Ser
149                   595                  600                   605
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151     Gly Lys Thr Ile Arg Glu Ala Tyr Ala Gln Arg Ile Pro Ser Gly Gly
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154     Asp Gly Lys Thr Leu Lys Phe Phe Gly Gln Ser Ile His Gly Glu Met
155     625                   630                  635                   640
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157     Asp Leu Asn Gly Asp Gly Leu Thr Asp Val Thr Ile Gly Gly Leu Gly
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159     gga gca gcc ctc ttc tgg gcc aga gat gtg gct gta gtt aaa gtg acc   2435
160     Gly Ala Ala Leu Phe Trp Ala Arg Asp Val Ala Val Val Lys Val Thr
161                   660                  665                   670
162     atg aat ttt gaa ccc aat aaa gtg aat att caa aag aaa aac tgc cgt   2483
163     Met Asn Phe Glu Pro Asn Lys Val Asn Ile Gln Lys Lys Asn Cys Arg
164                   675                  680                   685
165     gtg gag ggc aaa gaa aca gtg tgc ata aat gct aca atg tgt ttt cat   2531
166     Val Glu Gly Lys Glu Thr Val Cys Ile Asn Ala Thr Met Cys Phe His
167                   690                  695                   700
168     gtg aaa tta aag tct aaa gag gac tca att tac gag gct gat ctg cag   2579
169     Val Lys Leu Lys Ser Lys Glu Asp Ser Ile Tyr Glu Ala Asp Leu Gln
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171     tac cgt gtc acc ctt gat tca ctg agg cag ata tca cgg agc ttt ttt   2627
172     Tyr Arg Val Thr Leu Asp Ser Leu Arg Gln Ile Ser Arg Ser Phe Phe
173                   725                  730                   735
174     tct gga act cag gaa agg aag att caa aga aat atc acc gtt cga gaa   2675
175     Ser Gly Thr Gln Glu Arg Lys Ile Gln Arg Asn Ile Thr Val Arg Glu
176                   740                  745                   750
177     tca gaa tgc atc agg cac tcc ttc tac atg ttg gac aaa cat gac ttt   2723
178     Ser Glu Cys Ile Arg His Ser Phe Tyr Met Leu Asp Lys His Asp Phe
179                   755                  760                   765
180     cag gac tct gtg aga gtg act ctg gat ttt aat ctc act gat cca gaa   2771
181     Gln Asp Ser Val Arg Val Thr Leu Asp Phe Asn Leu Thr Asp Pro Glu
182                   770                  775                   780
183     aat ggt cct gta ctt gat gac gct ctg cca aac tca gtc cac gaa cac   2819
184     Asn Gly Pro Val Leu Asp Asp Ala Leu Pro Asn Ser Val His Glu His
185     785                   790                  795                   800
186     att ccc ttt gcc aaa gac tgt gga aac aag gaa aga tgc att tca gac   2867
187     Ile Pro Phe Ala Lys Asp Cys Gly Asn Lys Glu Arg Cys Ile Ser Asp
188                   805                  810                   815
189     ctc act ctg aat gtg tcc acc aca gaa aag agc ctg ctg atc gtc aag   2915
190     Leu Thr Leu Asn Val Ser Thr Thr Glu Lys Ser Leu Leu Ile Val Lys
191                   820                  825                   830
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192   tcc cag cat gac aag ttc aac gtt agc ctc acc gtc aaa aac aaa gga   2963
193   Ser Gln His Asp Lys Phe Asn Val Ser Leu Thr Val Lys Asn Lys Gly
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195   gac agt gcg tac aac acc agg aca gtg gtg cag cat tca cca aat ctg   3011
196   Asp Ser Ala Tyr Asn Thr Arg Thr Val Val Gln His Ser Pro Asn Leu
197           850                 855                 860
198   att ttt tcg gga att gag gag atc caa aaa gat agc tgt gaa tct aat   3059
199   Ile Phe Ser Gly Ile Glu Glu Ile Gln Lys Asp Ser Cys Glu Ser Asn
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202   Gln Asn Ile Thr Cys Arg Val Gly Tyr Pro Phe Leu Arg Ala Gly Glu
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208   Glu Asn Ala Ile Ile His Leu Ser Ala Thr Ser Asp Ser Glu Glu Pro
209           915                 920                 925
210   ctg gaa tct ctt aat gat aat gaa gta aat att tcc atc cca gta aaa   3251
211   Leu Glu Ser Leu Asn Asp Asn Glu Val Asn Ile Ser Ile Pro Val Lys
212           930                 935                 940
213   tat gaa gtt gga ctg cag ttt tac agt tct gcg agt gaa cat cac att   3299
214   Tyr Glu Val Gly Leu Gln Phe Tyr Ser Ser Ala Ser Glu His His Ile
215   945                 950                 955                 960
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217   Ser Val Ala Ala Asn Glu Thr Ile Pro Glu Phe Ile Asn Ser Thr Glu
218           965                 970                 975
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220   Asp Ile Gly Asn Glu Ile Asn Val Phe Tyr Thr Ile Arg Lys Arg Gly
221           980                 985                 990
222   cat ttc cca atg cca gaa ctt cag  ctg tca att tca ttc  ccc aat ttg   3443
223   His Phe Pro Met Pro Glu Leu Gln  Leu Ser Ile Ser Phe  Pro Asn Leu
224           995                 1000                1005
225   acg gca  gat ggt tat cct gta  ctg tac cca att gga  tgg tca tct   3488
226   Thr Ala  Asp Gly Tyr Pro Val  Leu Tyr Pro Ile Gly  Trp Ser Ser
227       1010                1015                1020
228   tca gat  aat gtg aac tgt aga  ccc cgg agc ctt gag  gac ccc ttt   3533
229   Ser Asp  Asn Val Asn Cys Arg  Pro Arg Ser Leu Glu  Asp Pro Phe
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233       1040                1045                1050
234   ctc aaa  aga ggc aca atc cag  gac tgc agt agt acg  tgt gga gtt   3623
235   Leu Lys  Arg Gly Thr Ile Gln  Asp Cys Ser Ser Thr  Cys Gly Val
236       1055                1060                1065
237   gcc acc  atc acg tgt agc ctc  ctt cct tcc gac ctg  agt caa gtg   3668
238   Ala Thr  Ile Thr Cys Ser Leu  Leu Pro Ser Asp Leu  Ser Gln Val
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 05/08/2002
PATENT APPLICATION: **US/09/000,004A**   TIME: 10:40:09

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Output Set: **N:\CRF3\05082002\I000004A.raw**

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VERIFICATION SUMMARY   DATE: 05/08/2002
PATENT APPLICATION: **US/09/000,004A**   TIME: 10:40:09

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